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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/749,637A

TIME: 12:16:51

Input Set : A:\227a-rsq.txt

Output Set: N:\CRF3\08162001\I749637A.raw

ENTERED

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3 <110> APPLICANT: University of Utah Research Foundation
4      Cognetix, Inc.
5      Olivera, Baldomero M.
6      Cartier, G. Edward
7      Watkins, Maren
8      Hillyard, David R.
9      McIntosh, J. Michael
10     Layer, Richard T.
11     Jones, Robert M.
13 <120> TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
15 <130> FILE REFERENCE: 2314-227
17 <140> CURRENT APPLICATION NUMBER: US 09/749,637A
18 <141> CURRENT FILING DATE: 2000-12-28
20 <150> PRIOR APPLICATION NUMBER: US 60/243,412
21 <151> PRIOR FILING DATE: 2000-10-27
23 <150> PRIOR APPLICATION NUMBER: US60/219,440
24 <151> PRIOR FILING DATE: 2000-07-20
26 <150> PRIOR APPLICATION NUMBER: US 60/214,263
27 <151> PRIOR FILING DATE: 2000-06-26
29 <150> PRIOR APPLICATION NUMBER: US 60/173,754
30 <151> PRIOR FILING DATE: 1999-12-30
32 <160> NUMBER OF SEQ ID NOS: 409
34 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 261
38 <212> TYPE: DNA
39 <213> ORGANISM: Conus gloriamaris
41 <220> FEATURE:
42 <221> NAME/KEY: CDS
43 <222> LOCATION: (1)..(231)
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47 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
48 1          5          10          15
50 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt      96
51 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
52          20          25          30
54 ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg      144
55 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
56          35          40          45
58 gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa      192
59 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
60          50          55          60
62 aac tgc tgc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaactacc      241
63 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
64 65          70          75
66 gtgatgtctt ctctccctc      261

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68 <210> SEQ ID NO: 2

69 <211> LENGTH: 77

70 <212> TYPE: PRT

71 <213> ORGANISM: Conus gloriamaris

73 <400> SEQUENCE: 2

74 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

75 1 5 10 15

77 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu

78 20 25 30

80 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg

81 35 40 45

83 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln

84 50 55 60

86 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val

87 65 70 75

89 <210> SEQ ID NO: 3

90 <211> LENGTH: 29

91 <212> TYPE: PRT

92 <213> ORGANISM: Conus gloriamaris

94 <220> FEATURE:

95 <221> NAME/KEY: SITE

96 <222> LOCATION: (1)..(29)

97 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residu

98 e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp

99 or bromo-Trp

101 <400> SEQUENCE: 3

W--> 102 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln

103 1 5 10 15

W--> 105 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val

106 20 25

108 <210> SEQ ID NO: 4

109 <211> LENGTH: 29

110 <212> TYPE: PRT

111 <213> ORGANISM: Conus gloriamaris

113 <220> FEATURE:

114 <221> NAME/KEY: SITE

115 <222> LOCATION: (1)..(29)

116 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residu

117 e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr

118 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospn

119 o-Tyr; Xaa at residue 22 may be Trp or bromo-Trp

121 <400> SEQUENCE: 4

W--> 122 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln

123 1 5 10 15

W--> 125 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val

126 20 25

128 <210> SEQ ID NO: 5

129 <211> LENGTH: 29

130 <212> TYPE: PRT

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131 <213> ORGANISM: Conus gloriamaris
133 <220> FEATURE:
134 <221> NAME/KEY: SITE
135 <222> LOCATION: (1)..(29)
136 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at
residu
137     e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
138     or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo
139     -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
141 <400> SEQUENCE: 5
W--> 142 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
143 1             5             10             15
W--> 145 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
146             20             25
148 <210> SEQ ID NO: 6
149 <211> LENGTH: 542
150 <212> TYPE: DNA
151 <213> ORGANISM: Conus omaria
153 <220> FEATURE:
154 <221> NAME/KEY: CDS
155 <222> LOCATION: (146)..(235)
157 <400> SEQUENCE: 6
158 gaagctggtgta cgctgcagg taccggctcg gaattcccg gtcgacatca tcatcatcga      60
160 tccatctgtc catccatcca ttcattcatt cgctgccaga ctataataaa cattcaagtc      120
162 tctctttctt tttgtgtctg acaga tgc atc agg atg tgc cgt aga gaa gct      172
163                               Ser Ile Arg Met Cys Arg Arg Glu Ala
164                               1             5
166 caa ctt tgt gat ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc      220
167 Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
168 10             15             20             25
170 gtt ttg gtc tgc gtc taaaactacc gtgatgtctt ctctcccct ctagtagtag      275
171 Val Leu Val Cys Val
172             30
174 taggcggcgg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt      335
176 ctatagtgtc acctaaatto aattcaactg ccgtcgtttt acaacgtcgt gactgggaaa      395
178 accctggcgt taccctaaatt aatcgccctg cagcacatcc ccctttcgcc agctggcgta      455
180 atagcgaaga ggcccgacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat      515
182 gggacgcgcc ctgtagcggc gcattat                                     542
184 <210> SEQ ID NO: 7
185 <211> LENGTH: 30
186 <212> TYPE: PRT
187 <213> ORGANISM: Conus omaria
189 <400> SEQUENCE: 7
190 Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
191 1             5             10             15
193 Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val
194             20             25             30
196 <210> SEQ ID NO: 8
197 <211> LENGTH: 27
198 <212> TYPE: PRT

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11 m 199 <213> ORGANISM: Conus omaria
201 <220> FEATURE:
202 <221> NAME/KEY: SITE
203 <222> LOCATION: (1)..(27)
204 <223> OTHER INFORMATION: Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue
205      ay be Pro or hydroxy-Pro
207 <400> SEQUENCE: 8
W--> 208 Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
209 1      5      10      15
211 Cys His Gly Leu Phe Cys Val Leu Val Cys Val
212      20      25
214 <210> SEQ ID NO: 9
215 <211> LENGTH: 346
216 <212> TYPE: DNA
217 <213> ORGANISM: Conus textile
219 <220> FEATURE:
220 <221> NAME/KEY: CDS
221 <222> LOCATION: (25)..(315)
223 <400> SEQUENCE: 9
224 ggcattacct aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt      51
225      Met Lys Leu Thr Cys Met Met Ile Val
226      1      5
228 gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc      99
229 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
230 10      15      20      25
232 aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag      147
233 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
234      30      35      40
236 aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc      195
237 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
238      45      50      55
240 gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa      243
241 Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys
242      60      65      70
244 gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg      291
245 Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp
246      75      80      85
248 tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat      345
249 Tyr Cys Val Val Leu Ser Cys Thr
250 90      95
252 c      346
254 <210> SEQ ID NO: 10
255 <211> LENGTH: 97
256 <212> TYPE: PRT
257 <213> ORGANISM: Conus textile
259 <400> SEQUENCE: 10
260 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
261 1      5      10      15
263 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Met Glu Asn Leu

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264          20          25          30
266 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His
267          35          40          45
269 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
270          50          55          60
272 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
273 65          70          75          80
275 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys
276          85          90          95
278 Thr
280 <210> SEQ ID NO: 11
281 <211> LENGTH: 31
282 <212> TYPE: PRT
283 <213> ORGANISM: Conus textile
285 <220> FEATURE:
286 <221> NAME/KEY: SITE
287 <222> LOCATION: (1)..(31)
288 <223> OTHER INFORMATION: Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4
may be
289 Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-
290 Glu; Xaa at residue 23 may be Trp or bromo-Trp; Xaa at residue 24
292 <220> FEATURE:
293 <221> NAME/KEY: SITE
294 <222> LOCATION: (1)..(31)
295 <223> OTHER INFORMATION: may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-
Tyr
296 or O-phospho-Tyr
298 <400> SEQUENCE: 11
W--> 299 Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
300 1          5          10          15
W--> 302 Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr
303          20          25          30
305 <210> SEQ ID NO: 12
306 <211> LENGTH: 265
307 <212> TYPE: DNA
308 <213> ORGANISM: Conus omaria
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (1)..(234)
314 <400> SEQUENCE: 12
315 atg aaa ctg acg tgc ctg atg atc gtt gcc gtg ctg tcc ttg acc ggc          48
316 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
317 1          5          10          15
319 tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt          96
320 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
321          20          25          30
323 ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg          144
324 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
325          35          40          45
327 aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa          192
328 Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\227a-rsq.txt

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L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
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L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
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L:951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:1648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

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L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69